

SEQUENCE LISTING

<110> KAO CORPORATION

<120> Alkali protease

<130> P

<150> JP 2003-106709

<151> 2003-04-10

<160> 10

<170> PatentIn Ver. 3.1

<210> 1

<211> 434

<212> PRT

<213> Bacillus sp. KSM-KP43

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Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly

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Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly

35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp

50	55	60	
Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly			
65	70	75	80
Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser			
	85	90	95
Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln			
	100	105	110
Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn			
	115	120	125
Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn			
	130	135	140
Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala			
145	150	155	160
Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala			
	165	170	175
Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe			
	180	185	190
Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg			
	195	200	205
Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly			
	210	215	220
Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe			
225	230	235	240
Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met			
	245	250	255
Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe			
	260	265	270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
 275 280 285  
 Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn  
 290 295 300  
 Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr  
 305 310 315 320  
 Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser  
 325 330 335  
 Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
 340 345 350  
 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu  
 355 360 365  
 Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp  
 370 375 380  
 Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu  
 385 390 395 400  
 Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val  
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<212> DNA

<213> *Bacillus* sp. KSM-KP43

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Met Arg	Lys Lys	Lys Lys	Val Phe	Leu Ser	Val Leu	Ser Ala	Ala	
-205			-200			-195		

gcg att	ttg tcg	act gtt	gcg tta	agt aat	cca tct	gca ggt	ggt	90
Ala Ile	Leu Ser	Thr Val	Ala Leu	Ser Asn	Pro Ser	Ala Gly	Gly	
-190			-185			-180		

gca agg	aat ttt	gat ctg	gat ttc	aaa gga	att cag	aca aca	act	135
Ala Arg	Asn Phe	Asp Leu	Asp Phe	Lys Gly	Ile Gln	Thr Thr	Thr	

-175	-170	-165	
gat gct aaa ggt ttc tcc aag cag ggg cag act ggt gct gct gct			180
Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala			
-160	-155	-150	
ttt ctg gtg gaa tct gaa aat gtg aaa ctc cca aaa ggt ttg cag			225
Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln			
-145	-140	-135	
aag aag ctt gaa aca gtc ccg gca aat aat aaa ctc cat att atc			270
Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile			
-130	-125	-120	
caa ttc aat gga cca att tta gaa gaa aca aaa cag cag ctg gaa			315
Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu			
-115	-110	-105	
aaa aca ggg gca aag att ctc gac tac ata cct gat tat gct tac att			363
Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile			
-100	-95	-90	
gtc gag tat gag ggc gat gtt aag tca gca aca agc acc att gag cac			411
Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His			
-85	-80	-75	-70
gtg gaa tcc gtg gag cct tat ttg ccg ata tac aga ata gat ccc cag			459

Val Glu Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln

-65

-60

-55

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Leu Phe Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp

-50

-45

-40

aca aag cag aaa aat aaa gag gtg caa tta aga ggc atc gaa caa atc 555

Thr Lys Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile

-35

-30

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gca caa ttc gca ata agc aat gat gtg cta tat att acg gca aag cct 603

Ala Gln Phe Ala Ile Ser Asn Asp Val Leu Tyr Ile Thr Ala Lys Pro

-20

-15

-10

gag tat aag gtg atg aat gat gtt gcg cgt gga att gtc aaa gcg gat 651

Glu Tyr Lys Val Met Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp

-5

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gtg gct cag agc agc tac ggg ttg tat gga caa gga cag atc gta gcg 699

Val Ala Gln Ser Ser Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala

15

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25

gtt gcc gat aca ggg ctt gat aca ggt cgc aat gac agt tcg atg cat 747

Val Ala Asp Thr Gly Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His

30

35

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gaa gcc ttc cgc ggg aaa att act gca tta tat gca ttg gga cgg acg 795

Glu Ala Phe Arg Gly Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr

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aat aat gcc aat gat acg aat ggt cat ggt acg cat gtg gct ggc tcc 843

Asn Asn Ala Asn Asp Thr Asn Gly His Gly Thr His Val Ala Gly Ser

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gta tta gga aac ggc tcc act aat aaa gga atg gcg cct cag gcg aat 891

Val Leu Gly Asn Gly Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn

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85

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cta gtc ttc caa tct atc atg gat agc ggt ggg gga ctt gga gga cta 939

Leu Val Phe Gln Ser Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu

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100

105

cct tcg aat ctg caa acc tta ttc agc caa gca tac agt gct ggt gcc 987

Pro Ser Asn Leu Gln Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala

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115

120

aga att cat aca aac tcc tgg gga gca gca gtg aat ggg gct tac aca 1035

Arg Ile His Thr Asn Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr

125

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135

aca gat tcc aga aat gtg gat gac tat gtg cgc aaa aat gat atg acg 1083

Thr Asp Ser Arg Asn Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr

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atc ctt ttc gct gcc ggg aat gaa gga ccg aac ggc gga acc atc agt	1131
Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser	
160 165 170	
gca cca ggc aca gct aaa aat gca ata aca gtc gga gct acg gaa aac	1179
Ala Pro Gly Thr Ala Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn	
175 180 185	
ctc cgc cca agc ttt ggg tct tat gcg gac aat atc aac cat gtg gca	1227
Leu Arg Pro Ser Phe Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala	
190 195 200	
cag ttc tct tca cgt gga ccg aca aag gat gga cgg atc aaa ccg gat	1275
Gln Phe Ser Ser Arg Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp	
205 210 215	
gtc atg gca ccg gga acg ttc ata cta tca gca aga tct tct ctt gca	1323
Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala	
220 225 230 235	
ccg gat tcc tcc ttc tgg gcg aac cat gac agt aaa tat gca tac atg	1371
Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met	
240 245 250	
ggt gga acg tcc atg gct aca ccg atc gtt gct gga aac gtg gca cag	1419
Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln	



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ctt cgt gag cat ttt gtg aaa aac aga ggc atc aca cca aag cct tct			1467
Leu Arg Glu His Phe Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser			
270	275	280	
cta tta aaa gcg gca ctg att gcc ggt gca gct gac atc ggc ctt ggc			1515
Leu Leu Lys Ala Ala Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly			
285	290	295	
tac ccg aac ggt aac caa gga tgg gga cga gtg aca ttg gat aaa tcc			1563
Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser			
300	305	310	315
ctg aac gtt gcc tat gtg aac gag tcc agt tct cta tcc acc agc caa			1611
Leu Asn Val Ala Tyr Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln			
320	325	330	
aaa gcg acg tac tcg ttt act gct act gcc ggc aag cct ttg aaa atc			1659
Lys Ala Thr Tyr Ser Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile			
335	340	345	
tcc ctg gta tgg tct gat gcc cct gcg agc aca act gct tcc gta acg			1707
Ser Leu Val Trp Ser Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr			
350	355	360	
ctt gtc aat gat ctg gac ctt gtc att acc gct cca aat ggc aca cag			1755

Leu Val Asn Asp Leu Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln

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375

tat gta gga aat gac ttt act tcg cca tac aat gat aac tgg gat ggc 1803

Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly

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390

395

cgc aat aac gta gaa aat gta ttt att aat gca cca caa agc ggg acg 1851

Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr

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tat aca att gag gta cag gct tat aac gta ccg gtt gga cca cag acc 1899

Tyr Thr Ile Glu Val Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr

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Phe Ser Leu Ala Ile Val Asn

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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